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O.G. FIG.	CLASS	SUBCLASS
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5 10
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys
* * * *
Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val

25 30
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Ser Tyr
* * * * *
Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr
Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Tyr

45 50
Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn
* * * *
Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp
* CDR
Pro Glu Gln Gly Leu Glu Trp Ile Gly Trp Ile Asp

65 70
Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg
* * * * *
Asp Pro Lys The Gln Gly Arg Val Thr Met Thr Arg
* * * * *
Asp Pro Lys Phe Gln Gly Lys Ala Ser Ile Thr Ser

85 90
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala
* *
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala

105 110
- - - - -
Thr Ser Ser Phe Asp Phe Trp Gly Gln Gly Thr Thr
CDR 3
Thr Ser Ser Phe Asp Phe Trp Gly Gln Gly Thr Thr
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FIG. 1B

O.G. FIG.	CLASS	SUBCLASS
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15 20
Lys Pro Gly Ala Ser Val Lys Val Human HV3 VH
Lys Pro Gly Ala Ser Val Lys Val "CDR Grafted" VH
* * *
Arg Pro Gly Ala Leu Val Lys Leu Murine 1308F VH

35 40
Tyr Met His Trp Val Arg Gln Ala
* *
Tyr Ile Tyr Trp Val Arg Gln Ala *
CDR 1 *
Tyr Ile Tyr Trp Val Lys Gln Arg

55 60
Pro Ser Gly Gly Ser Thr Ser Tyr
* * * *
Pro Glu Asn Gly Asn Thr Val Phe
2
Pro Glu Asn Gly Asn Thr Val Phe

75 80
Asp Thr Ser Thr Ser Thr Val Tyr
Asp Thr Ser Thr Ser Thr Val Tyr
* * *
Asp Thr Ser Ser Asn Thr Ala Tyr

95 100
Val Tyr Tyr Cys Ala
Val Tyr Tyr Cys Ala Tyr Tyr gly
Val Tyr Tyr Cys Ala Tyr Tyr Gly
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- - - - -
Leu Thr Val Ser Ser
Leu Thr Val Ser Ser

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FIG. 2A

O.G. FIG.	
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5 10
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser
* * *
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr
25 30
Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
* * *
Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Arg Tyr
CDR 1
Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Arg Tyr
45 50
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
* *
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Arg Ala Asn
* * *
Gly Lys Ser Pro Lys Thr Leu Ile His Arg Ala Asn
65 70
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
* * *
Arg PHE Ser Gly Ser Gly Ser Gly Gln Glu Tyr Ser
85 90
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
* * *
Asp Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Phe His
* * *
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Phe His
105
- - - - -
Gly Thr Lys Leu Glu Ile Lys
Gly Thr Lys Leu Glu Ile Lys

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FIG. 2B

O.G. FIG.	CLASS	SUBCLASS
	APPROVED BY	DRAFTSMAN

15 20
Ala Ser Val GLY Asp Arg Val Thr - Human K102 VL

Ala Ser Val Gly Asp Arg Val Thr - "CDR Grafted" VL
* * *

Val Ser Leu Gly Glu Arg Val Thr - Murine 1308F VL

35 40
Leu Ala Trp Tyr Gln Gln Lys Pro
*

Leu Asn Trp Tyr Gln Gln Lys Pro
*

Leu Asn Trp Phe Gln Gln Lys Pro

55 60
Ser Leu Glu Ser Gly Val Pro Ser
* * *

Arg Leu Val Asp Gly Val Pro Ser
CDR 2

Arg Leu Val Asp Gly Val Pro Ser

75 80
Leu Thr Ile Ser Ser Leu Gln Pro

Leu Thr Ile Ser Ser Leu Gln Pro
*

Leu Thr Ile Ser Ser Leu Glu Phe

95 100
Ser Tyr Ser - - -
* * *

Glu Phe Pro Tyr Thr Phe Gly Gly
CDR 3

Glu Phe Pro Tyr Thr Phe Gly Gly
<<V / J>>

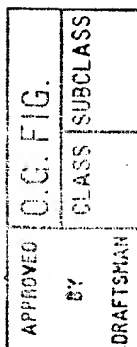


FIG. 3A

5' gcgaattccatggactggacctggagggtc 3'
MetAspTrpThrTrpArgValPheCysLeuLeuAlaValAlaProGlyAlaHisSerGln
5' ccATGGACTGGACCTGGAGGCTCTTCTGCTTGCTGGCTGTAGCACACAGGTGCCACTGCCAG
1-----+-----+-----+-----+-----+-----+-----+
3' TACCTGACCTGGACCTCCCAGAAAGACGACGACCGACATCGTGGTCCACGGGTGAGGGTC
ValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSerValLysValSer
GTGCAGCTGGTGCAGCTCTGGAGCTGAGGTGAAGAGCCCTGGAGCCTCAGTGAAGTTTCC
61-----+-----+-----+-----+-----+-----+-----+
CACGTCGACCACGTCAGACCTCGACTCCACTTCTTCGGACCTCGGAGTCACCTCCAAAGG
CysLysAlaSerGlyPheAsnIleLysAspTyrTyrIleTyrTrpValArgGlnAlaPro
TGCAAGGCATCTGGATTCAACATTAAAGGACTACTACATTACTGGGTGGCAGAGGCTCCT
121-----+-----+-----+-----+-----+-----+-----+
ACGTTCCGTAGACCTAAGTTGTAATTCCCTGATGATGTAATGACCCACGCTGTCCGAGGA

GlyGlnGlyLeuGluTrpNetGlyTrpIleAspProGluAsnGlyAsnThrValPheAsp
GGACAAGGCTCGAGTGGATGGATTGACCCCTGAGAAATGGTAATACTGTGTTTGAC
181-----+-----+-----+-----+-----+-----+-----+
CCTGTTCCCGAGCTCACCTACCCCAACCTAACTGGGACTCTTACCATTATGACACAAACTG

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FIG. 3B

ProLysPheGlnGlyArgValThrNetThrArgAspThrSerThrSerThrValTyrMet
CCGAAGTTCCAGGCGAGAGTCAACCATGACGAGGACACGTCACGAGCACAGTCTACATG
241-----+-----+-----+-----+-----+-----+-----+
GGCTTCAAGTCCCGTCTCAGTGGTACTGGTCCCTGTGCAGGTGCTCGTGTCAGATGTAC

GluLeuSerSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaTyrTyrGlyThr
GAGCTGAGCAGCCTGAGATCTGAGGACACGCGCGTGTATTACTGTGCGTACTACGGTACA
301-----+-----+-----+-----+-----+-----+-----+
CTCGACTCGTCGGACTCTAGACTCCTGTGCGCGCACATAATGACACGCATGATGCCATGT

SerSerPheAspPheTrpGlyGlnGlyThrThrLeuThrValSerSer
AGCTCCCTTTGACTTCTGGGGCCCAAGGCACCACTCTCACAGTGAGCTCA
361-----+-----+-----+-----+-----+-----+-----+

TCGAGGAAACTGAAGACCCCGGTTCCGTGGTGAGAGTGTCACTCGAGTattcctagg 5'
3' ggtgagagtgtcactcgagtattcctagggc

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[illegible]

valYhrIleThrCysLysAlaSerGlnAspIleAsnArgTyrLeuAsnTrpTyrGlnGln
GTCACCATCACTGGCAAGCGAGTCAGGACATTAATAGGTAGTTAAACTGGTACCAGCAG
-----+-----+-----+-----+-----+-----+-----+
121 CAGTGGTAGTGAACGTTCCGCTCAGTCCTGTAATTATCCATAAAATTTGACCATGGTCGTC

[illegible]

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIG. 4B

241 ProSerArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu
CCATCAAGGTCAGCGCAGTGGATCTGGACAGAAATTCACCTCTCACCATCAGCAGCCTG
-----+-----+-----+-----+-----+-----+
GGTAGTCCAAAGTCGCCGTACCTAGACCCCTGTCTTAAGTGAGAGTGTTAGTCGTCGGAC

301 GlnProAspPheAlaThrTyrTyrCysLeuGlnPheHisGluPheProTyrThrPhe
CAGCCTGATGATTTTGCAACTTATTACTGCCCTACAGTTTCATGAGTTCCCGTACACGTTT
-----+-----+-----+-----+-----+-----+
GTCGGACTACTAAACGTTGAATAATGACGGATGTCAAAGTACTCAAAGGCATGTGCAAG
3' gtgcaag

GlyGlyGlyThrLysLeuGluIleLys
GGAGGGGGACCAAGCTTGAAATAAAA 3'
-----+-----+-----

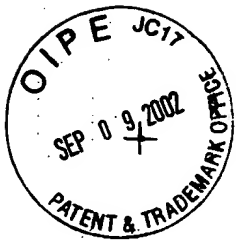
361 CCTCCCCCCTGGTTCGAACTTTATTTT 5'
cctccccctggttcgaacc 5'

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O.G. FIG.	
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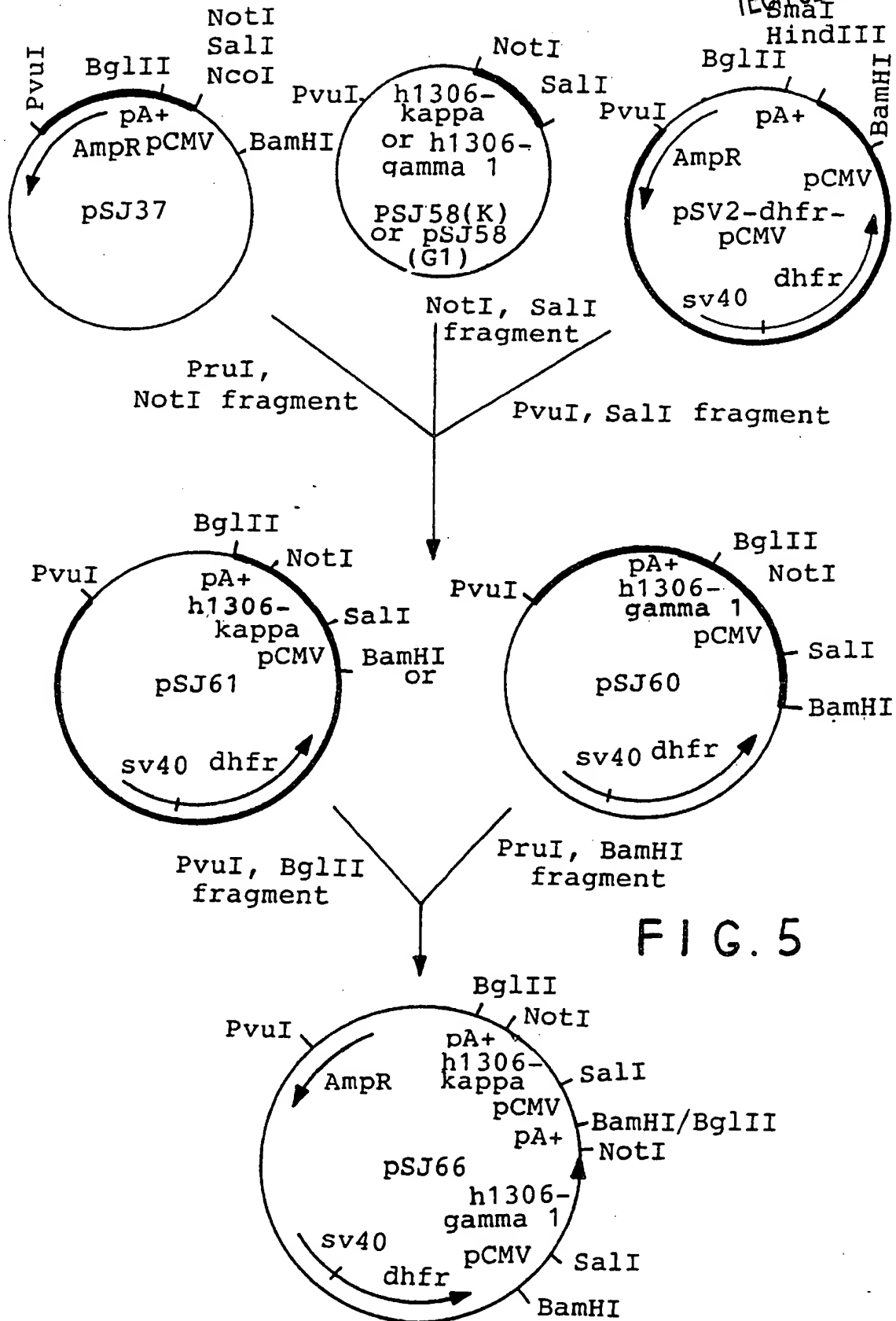


FIG. 5



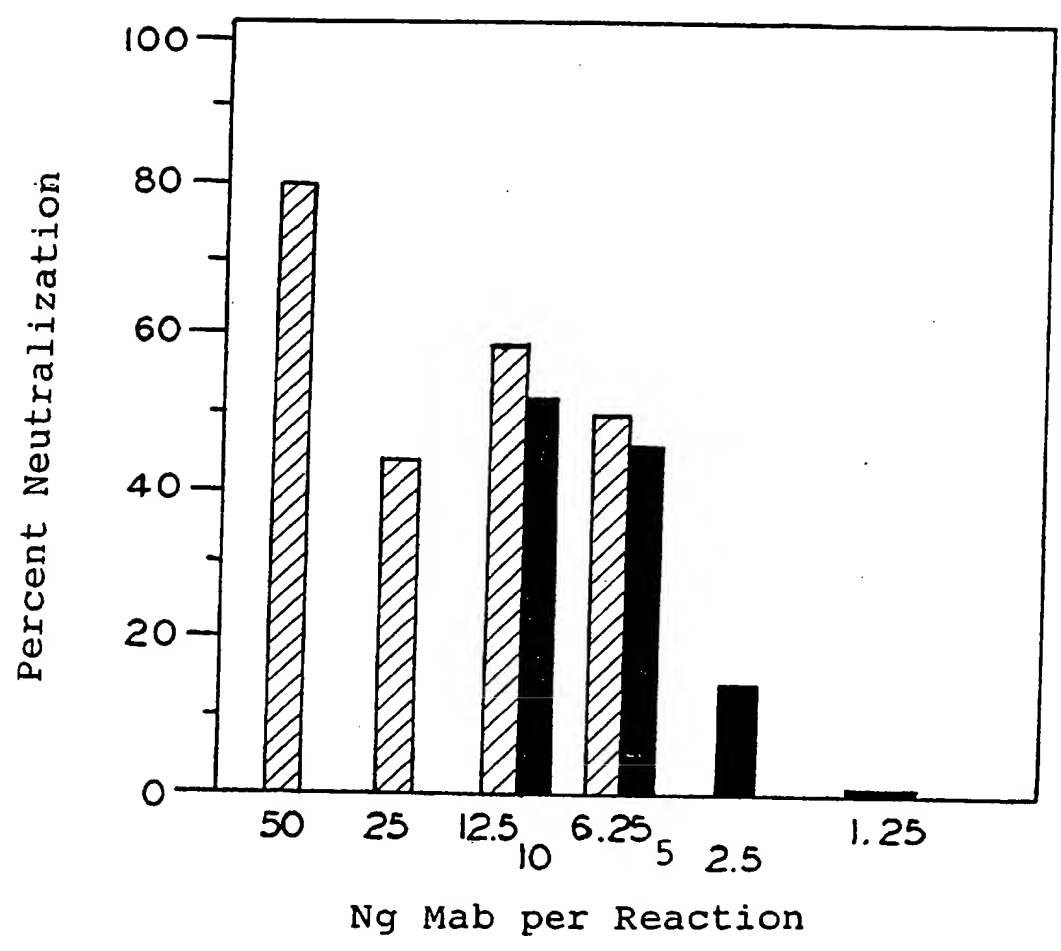
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O.G. FIG.		SUBCLASS	
CLASS			
APPROVED	BY	DRAFTSMAN	

FIG. 6

- Neut with Cos Hu
- ▨ Neut with 1308F Mu



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APPROVED	O.G.FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 7A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Human VH (Cor) 15

1 Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr "Humanized" VH 10
* * * * *

Gln Val Glu Leu Gln Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Murine 1129 VH

Gln Yhr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser

16 Gln Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser
* * * * *

Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser

Ser Ser Gly Met Cys Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
* * * * *

31 Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Pro Gly Lys
* * * * *

Thr Ser Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Glu

Ala Leu Glu Trp Leu Ala Asp Ile Glu Trp Asp Asp Lys Asp
* * * * *

46 Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Lys Lys Asp
* * * * *

Gly Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Lys Lys Asp

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIG. 7B

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Tyr Asn Thr Ser Leu Asp Thr Arg Leu Thr Ile Ser Lys Asp Thr
* * *
61 Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr
Swe Lys Asn Gln Val val Leu Thr Val Thr Asn Met Asp Pro Ala
*
76 Ser Lys Asn Gln Val val Leu Lys Val Thr Asn Met Asp Pro Ala
* * *
Ser Ser Asn Gln Val Phe Leu Lys Ile Thr Gly Val Asp Thr Ala
Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ile Yhr Val Ile Pro Ala Pro Ala Gly
* * * * *
91 Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp
Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp
Tyr Met Asp Val Trp Gly Arg Gly Thr Pro Val Thr Val Ser Ser
* * *
106 Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser



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APPROVED	O.G.FIG.	
BY	CLASS	SUBCLASS
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FIG. 8A

5	Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val	15	- Human K102 VL (SEQ ID 33)
	Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val *		- "CDR Grafted" VL (SEQ ID 34)
	Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro		- Murine 1129 VL (SEQ ID 35)
20	Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser	30	
	Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser *		
	Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Val Gly		
35	Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	45	
	Tyr Met His - Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys		
	Tyr Met His - Trp Tyr Gln Gln Lys Ser Ser Thr Ser Pro Lys		
50	Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser	60	
	Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser		
	Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly val Pro Gly		

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 8B

65 Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile 75
Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile
Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu Thr Ile
80 Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln 90
Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln
Ser Ser Ile Gln Ala Glu Asp Val Ala Thr Tyr Tyr Cys Phe Gln
95 Tyr Asn Ser Tyr Ser 100 105
* * *
Gly Ser Gly Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
CDR 3
Gly Ser Gly Tyr Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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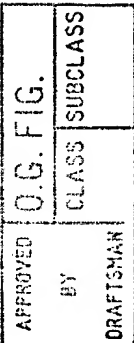


FIG. 9A

SJ153 5' -GGCGTCGACTCACC-

ATGGACTGGACCTGGAGGGTCTTCTGCTTGGCTGTAGCACCGGTGCCCACTCCC-3'

[illegible]

MetAspTrpThrTrpArgValPheCysLeuLeuAlaValAlaProGlyAlaHisSerGln

GTCACCTTAAGGGAGTCTGGTCCCTGGTGAAACCACACAGACCCCTCACACTGACC
61 -----+-----+-----+-----+-----+-----+-----+
 3' -GGAGGTGTGACTGG 120

ValThrLeuArgGluSerGlyProAlaLeuValLysProThrGlnThrLeuThrLeuThr

TGCACC-3' SJ151 5'- CAG
 121 -----+-----+-----+-----+-----+-----+-----+
 ACGTGGAGAGACCCAAAGTGACTCGTGAAGACCATACTCACATCCGACCTAAGCAGTC 180

CysThrPheSerGlyPheSerLeuSerThrSerGlyMetSerValGlyTrpIleArgGln

CCCCAGGGAAGCCCTGCACCTCGCTTGCAGACATTTGGTGGGATGACAAAAAGGACTAT
-----+-----+-----+-----+-----+-----+
GGGGTCCCCTTCGGG-5' SJ149 +-----+-----+-----+-----+-----+-----+ 240

3'- GATA

ProGlyLysAlaLeuGluTrpLeuAlaAspIleTrpTrpAspAspLysLysAspTyr

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		



FIG. 9B

241 AATCCATCCCCTGAAG-3' SJ152 5'-GGTC
 -----+-----+-----+-----+
 TTAGGTACCGACTTCTCGCGGAGGTGTAGAGGTTCCCTATGGAGGTTTGGTCCACCAG 300
 AsnProSerLeuLysSerArgLeuThrIleGerLysAspThrSerLysAsnGlnValVal

 301 CTTAAAGTGACCAACATGGACTCCTGCTGATACTGCCACTTACTGTGCTCGGTCTATG
 -----+-----+-----+-----+ 360
 GAATTTCACCTGGTTG-5' SJ148 3'-TAC
 LeuLysValThrAsnMetAspProAlaAspThrAlaThrTyrTyrCysAlaArgSerMet

 361 -----+-----+-----+-----+ 417
 TAGTGCTTGACCATGAAGCTACAGACCCCGCCCTGGTGCCAGTGGCAGTCCG-5' SJ147
 IleThrAsnTrpTyrPheAspValTrpGlyAlaGlyThrThrValThrValSerSer

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O.G. FIG.		
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FIG. 10

○ humanized 1129
● Chimeric 1129

